SEQUENCE LISTING

	(1) GENERAL INFORMATION:
5	(i) APPLICANT: Fuerst, Thomas R. McAtee, C. Patrick Yarbough, Patrice O. Zhang, Yifan
10	(ii) TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
	(iii) NUMBER OF SEQUENCES: 31
	(iv) CORRESPONDENCE ADDRESS:
15	(A) ADDRESSEE: Dehlinger & Associates
	(B) STREET: 350 Cambridge Ave., Suite 250
	(C) CITY: Palo Alto
	(D) STATE: CA
	(E) COUNTRY: USA
20	(F) ZIP: 94306
	(v) COMPUTER READABLE FORM:
	(A) MEDIUM TYPE: Floppy disk
	(B) COMPUTER: IBM PC compatible
25	(C) OPERATING SYSTEM: PC-DOS/MS-DOS
	(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
	(vi) CURRENT APPLICATION DATA:
	(A) APPLICATION NUMBER:
30	(B) FILING DATE:
	(C) CLASSIFICATION:
	(viii) ATTORNEY/AGENT INFORMATION:
	(A) NAME: Fabian, Gary R.
35	(B) REGISTRATION NUMBER: 33,875
	(C) REFERENCE/DOCKET NUMBER: 4600-0293.30
	(ix) TELECOMMUNICATION INFORMATION:
	(A) TELEPHONE: (415) 324-0880
40	(B) TELEFAX: (415) 324-0960

(2) INFORMATION FOR SEQ ID NO:1:

	1 3 1	STOTENCE	CHARACTERISTICS	
- 1		i amounder	CHARACIERISIICS	-

- (A) LENGTH: 2049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10

5

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
ORF-2

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	ATGCGCCCTC	GGCCTATTTT	GTTGCTGCTC	CTCATGTTTT	TGCCTATGCT	GCCGCGCCA	60
	CCGCCCGGTC	AGCCGTCTGG	CCGCCGTCGT	GGGCGCGCA	GCGGCGGTTC	CGGCGGTGGT	120
25	TTCTGGGGTG	ACCGGGTTGA	TTCTCAGCCC	TTCGCAATCC	CCTATATTCA	TCCAACCAAC	180
25	CCCTTCGCCC	CCGATGTCAC	CGCTGCGGCC	GGGGCTGGAC	CTCGTGTTCG	CCAACCCGCC	240
	CGACCACTCG	GCTCCGCTTG	GCGTGACCAG	GCCCAGCGCC	CCGCCGTTGC	CTCACGTCGT	300
30	AGACCTACCA	CAGCTGGGGC	CGCGCCGCTA	ACCGCGGTCG	CTCCGGCCCA	TGACACCCCG	360
	CCAGTGCCTG	ATGTCGACTC	CCGCGGCGCC	ATCTTGCGCC	GGCAGTATAA	CCTATCAACA	420
35	TCTCCCCTTA	CCTCTTCCGT	GGCCACCGGC	ACTAACCTGG	TTCTTTATGC	CGCCCCTCTT	480
35	AGTCCGCTTT	TACCCCTTCA	GGACGGCACC	AATACCCATA	TAATGGCCAC	GGAAGCTTCT	540
	AATTATGCCC	AGTACCGGGT	TGCCCGTGCC	ACAATCCGTT	ACCGCCCGCT	GGTCCCCAAT	600
40	GCTGTCGGCG	GTTACGCCAT	CTCCATCTCA	TTCTGGCCAC	AGACCACCAC	CACCCGACG	660

	TCCGTTGATA	TGAATTCAAT	AACCTCGACG	GATGTTCGTA	TTTTAGTCCA	GCCCGCCATA	720
	GCCTCTGAGC	TTGTGATCCC	AAGTGAGCGC	CTACACTATC	GTAACCAAGG	CTGGCGCTCC	780
5	GTCGAGACCT	CTGGGGTGGC	TGAGGAGGAG	GCTACCTCTG	GTCTTGTTAT	GCTTTGCATA	840
	CATGGCTCAC	TCGTAAATTC	CTATACTAAT	ACACCCTATA	CCGGTGCCCT	CGGGCTGTTG	900
10	GACTTTGCCC	TTGAGCTTGA	GTTTCGCAAC	CTTACCCCCG	GTAACACCAA	TACGCGGGTC	960
10	TCCCGTTATT	CCAGCACTGC	TCGCCACCGC	CTTCGTCGCG	GTGCGGACGG	GACTGCCGAG	1020
	CTCACCACCA	CGGCTGCTAC	CCGCTTTATG	AAGGACCTCT	ATTTTACTAG	TACTAATGGT	1080
15	GTCGGTGAGA	TCGGCCGCGG	GATAGCCCTC	ACCCTGTTCA	ACCTTGCTGA	CACTCTGCTT	1140
	GGCGGCCTGC	CGACAGAATT	GATTTCGTCG	GCTGGTGGCC	AGCTGTTCTA	CTCCCGTCCC	1200
20	GTTGTCTCAG	CCAATGGCGA	GCCGACTGTT	AAGTTGTATA	CATCTGTAGA	GAATGCTCAG	1260
20	CAGGATAAGG	GTATTGCAAT	CCCGCATGAC	ATTGACCTCG	GAGAATCTCG	TGTGGTTATT	1320
	CAGGATTATG	ATAACCAACA	TGAACAAGAT	CGGCCGACGC	CTTCTCCAGC	CCCATCGCGC	1380
25	CCTTTCTCTG	TCCTTCGAGC	TAATGATGTG	CTTTGGCTCT	CTCTCACCGC	TGCCGAGTAT	1440
	GACCAGTCCA	CTTATGGCTC	TTCGACTGGC	CCAGTTTATG	TTTCTGACTC	TGTGACCTTG	1500
30	GTTAATGTTG	CGACCGGCGC	GCAGGCCGTT	GCCCGGTCGC	TCGATTGGAC	CAAGGTCACA	1560
30	CTTGACGGTC	GCCCCTCTC	CACCATCCAG	CAGTACTCGA	AGACCTTCTT	TGTCCTGCCG	1620
	CTCCGCGGTA	AGCTCTCTTT	CTGGGAGGCA	GGCACAACTA	AAGCCGGGTA	CCCTTATAAT	1680
35	TATAACACCA	CTGCTAGCGA	CCAACTGCTT	GTCGAGAATG	CCGCCGGGCA	CCGGGTCGCT	1740
	ATTTCCACTT	ACACCACTAG	CCTGGGTGCT	GGTCCCGTCT	CCATTTCTGC	GGTTGCCGTT	1800
40	TTAGCCCCCC	ACTCTGCGCT	AGCATTGCTT	GAGGATACCT	TGGACTACCC	TGCCCGCGCC	1860
4 0	CATACTTTTG	ATGATTTCTG	CCCAGAGTGC	CGCCCCTTG	GCCTTCAGGG	CTGCGCTTTC	1920

	CAGTCTACTG TCGCTGAGCT TCAGCGCCTT AAGATGAAGG TGGGTAAAAC TCGGGAGTTG	1980
	TAGTTTATTT GCTTGTGCCC CCCTTCTTTC TGTTGCTTAT TTCTCATTTC TGCGTTCCGC	2040
5	GCTCCCTGA	2049
	(2) INFORMATION FOR SEQ ID NO:2:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2058 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
20	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain) ORF-2 region</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
25	ATGCGCCCTA GGCCTCTTTT GCTGTTGTTC CTCTTGTTTC TGCCTATGTT GCCCGCGCCA	60
	CCGACCGGTC AGCCGTCTGG CCGCCGTCGT GGGCGGCGCA GCGGCGGTAC CGGCGGTGGT	120
30	TTCTGGGGTG ACCGGGTTGA TTCTCAGCCC TTCGCAATCC CCTATATTCA TCCAACCAAC	180
30	CCCTTTGCCC CAGACGTTGC CGCTGCGTCC GGGTCTGGAC CTCGCCTTCG CCAACCAGCC	240
	CGGCCACTTG GCTCCACTTG GCGAGATCAG GCCCAGCGCC CCTCCGCTGC CTCCCGTCGC	300
35	CGACCTGCCA CAGCCGGGGC TGCGGCGCTG ACGGCTGTGG CGCCTGCCCA TGACACCTCA	360
	CCCGTCCCGG ACGTTGATTC TCGCGGTGCA ATTCTACGCC GCCAGTATAA TTTGTCTACT	420
40	TCACCCCTGA CATCCTCTGT GGCCTCTGGC ACTAATTTAG TCCTGTATGC AGCCCCCCTT	480
. •	AATCCGCCTC TGCCGCTGCA GGACGGTACT AATACTCACA TTATGGCCAC AGAGGCCTCC	540

AATTATGCAC	AGTACCGGGT	TGCCCGCGCT	ACTATCCGTT	ACCGGCCCT	AGTGCCTAAT	600
GCAGTTGGAG	GCTATGCTAT	ATCCATTTCT	TTCTGGCCTC	AAACAACCAC	C AACCCCTACA	660
TCTGTTGACA	TGAATTCCAT	TACTTCCACT	GATGTCAGGA	TTCTTGTTCA	ACCTGGCATA	720
GCATCTGAAT	TGGTCATCCC	AAGCGAGCGC	CTTCACTACC	GCAATCAAGG	TTGGCGCTCG	780
GTTGAGACAT	CTGGTGTTGC	TGAGGAGGAA	GCCACCTCCG	GTCTTGTCAT	GTTATGCATA	840
CATGGCTCTC	CAGTTAACTC	CTATACCAAT	ACCCCTTATA	CCGGTGCCCT	TGGCTTACTG	900
GACTTTGCCT	TAGAGCTTGA	GTTTCGCAAT	CTCACCACCT	GTAACACCAA	TACACGTGTG	960
TCCCGTTACT	CCAGCACGGC	CCGTCACCGG	CTCCGCCGAG	GGGCCGACGG	GACTGCGGAG	1020
CTGACCACAA	CTGCAGCCAC	CAGGTTCATG	AAAGATCTCC	ACTTTACCGG	CCTTAATGGG	1080
GTAGGTGAAG	TCGGCCGCGG	GATAGCTCTA	ACATTACTTA	ACCTTGCTGA	CACGCTCCTC	1140
GGCGGGCTCC	CGACAGAATT	AATTTCGTCG	GCTGGCGGGC	AACTGTTTTA	TTCCCGCCCG	1200
GTTGTCTCAG	CCAATGGCGA	GCCAACCGTG	AAGCTCTATA	CATCAGTGGA	GAATGCTCAG	1260
CAGGATAAGG	GTGTTGCTAT	CCCCCACGAT	ATCGATCTTG	GTGATTCGCG	TGTGGTCATT	1320
CAGGATTATG	ACAACCAGCA	TGAGCAGGAT	CGGCCCACCC	CGTCGCCTGC	GCCATCTCGG	1380
CCTTTTTCTG	TTCTCCGAGC	AAATGATGTA	CTTTGGCTGT	CCCTCACTGC	AGCCGAGTAT	1440
GACCAGTCCA	CTTACGGGTC	GTCAACTGGC	CCGGTTTATA	TCTCGGACAG	CGTGACTTTG	1500
GTGAATGTTG	CGACTGGCGC	GCAGGCCGTA	GCCCGATCGC	TTGACTGGTC	CAAAGTCACC	1560
CTCGACGGGC	GGCCCCTCCC	GACTGTTGAG	CAATATTCCA	AGACATTCTT	TGTGCTCCCC	1620
CTTCGTGGCA	AGCTCTCCTT	TTGGGAGGCC	GGCACAACAA	AAGCAGGTTA	TCCTTATAAT	1680
ТАТААТАСТА	CTGCTAGTGA	CCAGATTCTG	ATTGAAAATG	CTGCCGGCCA	TCGGGTCGCC	1740
ATTTCAACCT	ATACCACCAG	GCTTGGGGCC	GGTCCGGTCG	CCATTTCTGC	GGCCGCGGTT	1800

	TTGGCTCCAC GCTCCGCCCT GGCTCTGCTG GAGGATACTT TTGATTATCC GGGGCGGCG	1860
	CACACATTTG ATGACTTCTG CCCTGAATGC CGCGCTTTAG GCCTCCAGGG TTGTGCTTTC	1920
5	CAGTCAACTG TCGCTGAGCT CCAGCGCCTT AAAGTTAAGG TGGGTAAAAC TCGGGAGTTG	1980
	TAGTTTATTT GGCTGTGCCC ACCTACTTAT ATCTGCTGAT TTCCTTTATT TCCTTTTCT	2040
10	CGGTCCCGCG CTCCCTGA	2058
10	(2) INFORMATION FOR SEQ ID NO:3:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1647 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
25	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma) r62kDa,</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
30	GCGGTCGCTC CGGCCCATGA CACCCCGCCA GTGCCTGATG TCGACTCCCG CGGCGCCATC	60
	TTGCGCCGGC AGTATAACCT ATCAACATCT CCCCTTACCT CTTCCGTGGC CACCGGCACT	120
35	AACCTGGTTC TTTATGCCGC CCCTCTTAGT CCGCTTTTAC CCCTTCAGGA CGGCACCAAT	180
33	ACCCATATAA TGGCCACGGA AGCTTCTAAT TATGCCCAGT ACCGGGTTGC CCGTGCCACA	240
	ATCCGTTACC GCCCGCTGGT CCCCAATGCT GTCGGCGGTT ACGCCATCTC CATCTCATTC	300
40	TGGCCACAGA CCACCACCAC CCCGACGTCC GTTGATATGA ATTCAATAAC CTCGACGGAT	360

	GTTCGTATTT	TAGTCCAGCC	CGGCATAGCC	TCTGAGCTTG	TGATCCCAAG	TGAGCGCCTA	420
	CACTATCGTA	ACCAAGGCTG	GCGCTCCGTC	GAGACCTCTG	GGGTGGCTGA	GGAGGAGGCT	480
5	ACCTCTGGTC	TTGTTATGCT	TTGCATACAT	GGCTCACTCG	талаттсста	TACTAATACA	540
	CCCTATACCG	GTGCCCTCGG	GCTGTTGGAC	TTTGCCCTTG	AGCTTGAGTT	TCGCAACCTT	600
10	ACCCCGGTA	ACACCAATAC	GCGGGTCTCC	CGTTATTCCA	GCACTGCTCG	CCACCGCCTT	660
10	CGTCGCGGTG	CGGACGGGAC	TGCCGAGCTC	ACCACCACGG	CTGCTACCCG	CTTTATGAAG	720
	GACCTCTATT	TTACTAGTAC	TAATGGTGTC	GGTGAGATCG	GCCGCGGGAT	AGCCCTCACC	780
15	CTGTTCAACC	TTGCTGACAC	TCTGCTTGGC	GGCCTGCCGA	CAGAATTGAT	TTCGTCGGCT	840
	GGTGGCCAGC	TGTTCTACTC	CCGTCCCGTT	GTCTCAGCCA	ATGGCGAGCC	GACTGTTAAG	900
20	TTGTATACAT	CTGTAGAGAA	TGCTCAGCAG	GATAAGGGTA	TTGCAATCCC	GCATGACATT	960
20	GACCTCGGAG	AATCTCGTGT	GGTTATTCAG	GATTATGATA	ACCAACATGA	ACAAGATCGG	1020
	CCGACGCCTT	CTCCAGCCCC	ATCGCGCCCT	TTCTCTGTCC	TTCGAGCTAA	TGATGTGCTT	1080
25	TGGCTCTCTC	TCACCGCTGC	CGAGTATGAC	CAGTCCACTT	ATGGCTCTTC	GACTGGCCCA	1140
	GTTTATGTTT	CTGACTCTGT	GACCTTGGTT	AATGTTGCGA	CCGGCGCGCA	GGCCGTTGCC	1200
30	CGGTCGCTCG	ATTGGACCAA	GGTCACACTT	GACGGTCGCC	CCCTCTCCAC	CATCCAGCAG	1260
30	TACTCGAAGA	CCTTCTTTGT	CCTGCCGCTC	CGCGGTAAGC	TCTCTTTCTG	GGAGGCAGGC	1320
	ACAACTAAAG	CCGGGTACCC	TTATAATTAT	AACACCACTG	CTAGCGACCA	ACTGCTTGTC	1380
35	GAGAATGCCG	CCGGGCACCG	GGTCGCTATT	TCCACTTACA	CCACTAGCCT	GGGTGCTGGT	1440
	CCCGTCTCCA	TTTCTGCGGT	TGCCGTTTTA	GCCCCCACT	CTGCGCTAGC	ATTGCTTGAG	1500
4.0	GATACCTTGG	ACTACCCTGC	CCGCGCCCAT	ACTTTTGATG	ATTTCTGCCC	AGAGTGCCGC	1560
40	CCCCTTGGCC	TTCAGGGCTG	CGCTTTCCAG	TCTACTGTCG	CTGAGCTTCA	GCGCCTTAAG	1620

1647	
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(2) INFORMAT	ION F	OR .	SEO	ID	NO:4:
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5	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1647 base pair
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain) r62kDa, FIGURE 2

20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:													
	GCTGTGGCGC	CTGCCCATGA	CACCTCACCC	GTCCCGGACG	TTGATTCTCG	CGGTGCAATT	60							
	CTACGCCGCC	AGTATAATTT	GTCTACTTCA	CCCCTGACAT	CCTCTGTGGC	CTCTGGCACT	120							
25	AATTTAGTCC	TGTATGCAGC	CCCCCTTAAT	CCGCCTCTGC	CGCTGCAGGA	CGGTACTAAT	180							
	ACTCACATTA	TGGCCACAGA	GGCCTCCAAT	TATGCACAGT	ACCGGGTTGC	CCGCGCTACT	240							
30	ATCCGTTACC	GGCCCCTAGT	GCCTAATGCA	GTTGGAGGCT	ATGCTATATC	CATTTCTTTC	300							
	TGGCCTCAAA	CAACCACAAC	CCCTACATCT	GTTGACATGA	ATTCCATTAC	TTCCACTGAT	360							
	GTCAGGATTC	TTGTTCAACC	TGGCATAGCA	TCTGAATTGG	TCATCCCAAG	CGAGCGCCTT	420							
35	CACTACCGCA	ATCAAGGTTG	GCGCTCGGTT	GAGACATCTG	GTGTTGCTGA	GGAGGAAGCC	480							
	ACCTCCGGTC	TTGTCATGTT	ATGCATACAT	GGCTCTCCAG	TTAACTCCTA	TACCAATACC	540							
40	CCTTATACCG	GTGCCCTTGG	CTTACTGGAC	TTTGCCTTAG	AGCTTGAGTT	TCGCAATCTC	600							
40	ACCACCTGTA	ACACCAATAC	ACGTGTGTCC	CGTTACTCCA	GCACGGCCCG	TCACCGGCTC	660							

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	CGCCGAGGGG	CCGACGGGAC	TGCGGAGCTG	ACCACAACTG	CAGCCACCAG	GTTCATGAAA	720
	GATCTCCACT	TTACCGGCCT	TAATGGGGTA	GGTGAAGTCG	GCCGCGGGAT	AGCTCTAACA	780
5	TTACTTAACC	TTGCTGACAC	GCTCCTCGGC	GGGCTCCCGA	CAGAATTAAT	TTCGTCGGCT	840
	GGCGGGCAAC	TGTTTTATTC	CCGCCCGGTT	GTCTCAGCCA	ATGGCGAGCC	AACCGTGAAG	900
10	CTCTATACAT	CAGTGGAGAA	TGCTCAGCAG	GATAAGGGTG	TTGCTATCCC	CCACGATATC	960
10	GATCTTGGTG	ATTCGCGTGT	GGTCATTCAG	GATTATGACA	ACCAGCATGA	GCAGGATCGG	1020
	CCCACCCCGT	CGCCTGCGCC	ATCTCGGCCT	TTTTCTGTTC	TCCGAGCAAA	TGATGTACTT	1080
15	TGGCTGTCCC	TCACTGCAGC	CGAGTATGAC	CAGTCCACTT	ACGGGTCGTC	AACTGGCCCG	1140
	GTTTATATCT	CGGACAGCGT	GACTTTGGTG	AATGTTGCGA	CTGGCGCGCA	GGCCGTAGCC	1200
20	CGATCGCTTG	ACTGGTCCAA	AGTCACCCTC	GACGGGCGGC	CCCTCCCGAC	TGTTGAGCAA	1260
20	TATTCCAAGA	CATTCTTTGT	GCTCCCCCTT	CGTGGCAAGC	TCTCCTTTTG	GGAGGCCGGC	1320
	ACAACAAAAG	CAGGTTATCC	TATAATTAT	AATACTACTG	CTAGTGACCA	GATTCTGATT	1380
25	GAAAATGCTG	CCGGCCATCG	GGTCGCCATT	TCAACCTATA	CCACCAGGCT	TGGGGCCGGT	1440
	CCGGTCGCCA	TTTCTGCGGC	CGCGGTTTTG	GCTCCACGCT	CCGCCCTGGC	TCTGCTGGAG	1500
30	GATACTTTTG	ATTATCCGGG	GCGGGCGCAC	ACATTTGATG	ACTTCTGCCC	TGAATGCCGC	1560
30	GCTTTAGGCC	TCCAGGGTTG	TGCTTTCCAG	TCAACTGTCG	CTGAGCTCCA	GCGCCTTAAA	1620
	GTTAAGGTGG	GTAAAACTCG	GGAGTTG				1647

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 984 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 5 (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3 region

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGCGGACG	GGACTGCCGA	GCTCACCACC	ACGGCTGCTA	CCCGCTTTAT	GAAGGACCTC	60
TATTTTACTA	GTACTAATGG	TGTCGGTGAG	ATCGGCCGCG	GGATAGCCCT	CACCCTGTTC	120
AACCTTGCTG	ACACTCTGCT	TGGCGGCCTG	CCGACAGAAT	TGATTTCGTC	GGCTGGTGGC	180
CAGCTGTTCT	ACTCCCGTCC	CGTTGTCTCA	GCCAATGGCG	AGCCGACTGT	TAAGTTGTAT	240
ACATCTGTAG	AGAATGCTCA	GCAGGATAAG	GGTATTGCAA	TCCCGCATGA	CATTGACCTC	300
GGAGAATCTC	GTGTGGTTAT	TCAGGATTAT	GATAACCAAC	ATGAACAAGA	TCGGCCGACG	360
CCTTCTCCAG	CCCCATCGCG	CCCTTTCTCT	GTCCTTCGAG	CTAATGATGT	GCTTTGGCTC	420
TCTCTCACCG	CTGCCGAGTA	TGACCAGTCC	ACTTATGGCT	CTTCGACTGG	CCCAGTTTAT	480
GTTTCTGACT	CTGTGACCTT	GGTTAATGTT	GCGACCGGCG	CGCAGGCCGT	TGCCCGGTCG	540
CTCGATTGGA	CCAAGGTCAC	ACTTGACGGT	CGCCCCTCT	CCACCATCCA	GCAGTACTCG	600
AAGACCTTCT	TTGTCCTGCC	GCTCCGCGGT	AAGCTCTCTT	TCTGGGAGGC	AGGCACAACT	660
AAAGCCGGGT	ACCCTTATAA	TTATAACACC	ACTGCTAGCG	ACCAACTGCT	TGTCGAGAAT	720
GCCGCCGGGC	ACCGGGTCGC	TATTTCCACT	TACACCACTA	GCCTGGGTGC	TGGTCCCGTC	780
TCCATTTCTG	CGGTTGCCGT	TTTAGCCCCC	CACTCTGCGC	TAGCATTGCT	TGAGGATACC	840
TTGGACTACC	CTGCCCGCGC	CCATACTTTT	GATGATTTCT	GCCCAGAGTG	CCGCCCCCTT	900

	GGCCTTCAGG GCTGCGCTTT CCAGTCTACT GTCGCTGAGC TTCAGCGCCT TAAGATGAAG	960
	GTGGGTAAAA CTCGGGAGTT GTAG	984
5	(2) INFORMATION FOR SEQ ID NO:6:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 984 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(iii) HYPOTHETICAL: NO	
20	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatits E Virus (Mexico strain) s region</pre>	5 G 3
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
25	GGGGCCGACG GGACTGCGGA GCTGACCACA ACTGCAGCCA CCAGGTTCAT GAAAGATCTC	60
23	CACTTTACCG GCCTTAATGG GGTAGGTGAA GTCGGCCGCG GGATAGCTCT AACATTACTT	120
	AACCTTGCTG ACACGCTCCT CGGCGGGCTC CCGACAGAAT TAATTTCGTC GGCTGGCGGG	180
30	CAACTGTTTT ATTCCCGCCC GGTTGTCTCA GCCAATGGCG AGCCAACCGT GAAGCTCTAT	240
	ACATCAGTGG AGAATGCTCA GCAGGATAAG GGTGTTGCTA TCCCCCACGA TATCGATCTT	300
35	GGTGATTCGC GTGTGGTCAT TCAGGATTAT GACAACCAGC ATGAGCAGGA TCGGCCCACC	360
	CCGTCGCCTG CGCCATCTCG GCCTTTTTCT GTTCTCCGAG CAAATGATGT ACTTTGGCTG	420
	TCCCTCACTG CAGCCGAGTA TGACCAGTCC ACTTACGGGT CGTCAACTGG CCCGGTTTAT	480
40	ATCTCGGACA GCGTGACTTT GGTGAATGTT GCGACTGGCG CGCAGGCCGT AGCCCGATCG	540

	CTTGACTGGT CCAAAGTCAC CCTCGACGGG CGGCCCCTCC CGACTGTTGA GCAATATTCC	600												
	AAGACATTCT TTGTGCTCCC CCTTCGTGGC AAGCTCTCCT TTTGGGAGGC CGGCACAACA	660												
5	AAAGCAGGTT ATCCTTATAA TTATAATACT ACTGCTAGTG ACCAGATTCT GATTGAAAAT	720												
	GCTGCCGGCC ATCGGGTCGC CATTTCAACC TATACCACCA GGCTTGGGGC CGGTCCGGTC	780												
10	GCCATTTCTG CGGCCGCGT TTTGGCTCCA CGCTCCGCCC TGGCTCTGCT GGAGGATACT	840												
10	TTTGATTATC CGGGGCGGC GCACACATTT GATGACTTCT GCCCTGAATG CCGCGCTTTA	900												
	GGCCTCCAGG GTTGTGCTTT CCAGTCAACT GTCGCTGAGC TCCAGCGCCT TAAAGTTAAG	960												
15	GTGGGTAAAA CTCGGGAGTT GTAG	984												
	(2) INFORMATION FOR SEQ ID NO:7:													
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 147 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear													
25	(ii) MOLECULE TYPE: DNA (genomic)													
	(iii) HYPOTHETICAL: NO													
30	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) 406.3-2</pre>													
3.5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:													
- •	ACCTTGGACT ACCCTGCCCG CGCCCATACT TTTGATGATT TCTGCCCAGA GTGCCGCCCC	60												
	CTTGGCCTTC AGGGCTGCGC TTTCCAGTCT ACTGTCGCTG AGCTTCAGCG CCTTAAGATG	120												
10	AAGGTGGGTA AAACTCGGGA GTTGTAG	147												

	(2) INFORMATION FOR SEQ ID NO:8:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 147 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
15	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
20	ACTTTTGATT ATCCGGGGCG GGCGCACACA TTTGATGACT TCTGCCCTGA ATGCCGCGCT	60
	TTAGGCCTCC AGGGTTGTGC TTTCCAGTCA ACTGTCGCTG AGCTCCAGCG CCTTAAAGTT	120
25	AAGGTGGGTA AAACTCGGGA GTTGTAG	147
	(2) INFORMATION FOR SEQ ID NO:9:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 372 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) forelogi. Timear	
2 =	(ii) MOLECULE TYPE: DNA (genomic)	
35	(iii) HYPOTHETICAL: NO	
	(vi) ORIGINAL SOURCE:	
40	(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma Strain) ORF-3 region	
70	one o region	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
	ATGAATAACA TGTCTTTTGC TGCGCCCATG GGTTCGCGAC CATGCGCCCT CGGCCTATTT	60
5	TGTTGCTGCT CCTCATGTTT TTGCCTATGC TGCCCGCGCC ACCGCCCGGT CAGCCGTCTG	120
	GCCGCCGTCG TGGGCGCCC AGCGGCGGTT CCGGCGGTGG TTTCTGGGGT GACCGGGTTG	180
	ATTCTCAGCC CTTCGCAATC CCCTATATTC ATCCAACCAA CCCCTTCGCC CCCGATGTCA	240
LO	CCGCTGCGGC CGGGGCTGGA CCTCGTGTTC GCCAACCCGC CCGACCACTC GGCTCCGCTT	300
	GGCGTGACCA GGCCCAGCGC CCCGCCGTTG CCTCACGTCG TAGACCTACC ACAGCTGGGG	360
15	CCGCGCCGCT AA	372
	(2) INFORMATION FOR SEQ ID NO:10:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 372 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
30	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
35	ATGAATAACA TGTGGTTTGC TGCGCCCATG GGTTCGCCAC CATGCGCCCT AGGCCTCTTT	60
	TGCTGTTGTT CCTCTTGTTT CTGCCTATGT TGCCCGCGCC ACCGACCGGT CAGCCGTCTG	120
4 0	GCCGCCGTCG TGGGCGGCGC AGCGGCGGTA CCGGCGGTGG TTTCTGGGGT GACCGGGTTG	180

	ATTCTCAGCC CTTCGCAATC CCCTATATTC ATCCAACCAA CCCCTTTGCC CCAGACGTTG	240
	CCGCTGCGTC CGGGTCTGGA CCTCGCCTTC GCCAACCAGC CCGGCCACTT GGCTCCACTT	300
5	GGCGAGATCA GGCCCAGCGC CCCTCCGCTG CCTCCCGTCG CCGACCTGCC ACAGCCGGGG	360
	CTGCGGCGCT GA	372
10	(2) INFORMATION FOR SEQ ID NO:11:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 99 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(iii) HYPOTHETICAL: NO	
	(vi) ORIGINAL SOURCE:	
	(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)	
	406.4-2 region	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
	GCCAACCCGC CCGACCACTC GGCTCCGCTT GGCGTGACCA GGCCCAGCGC CCCGCCGTTG	60
30	CCTCACGTCG TAGACCTACC ACAGCTGGGG CCGCGCCGC	99
	(2) INFORMATION FOR SEQ ID NO:12:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 99 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	

	(iii) HYPOTHETICAL: NO	
5	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
10	GCCAACCAGC CCGGCCACTT GGCTCCACTT GGCGAGATCA GGCCCAGCGC CCCTCCGCTG	60
	CCTCCCGTCG CCGACCTGCC ACAGCCGGGG CTGCGGCGC	99
15	(2) INFORMATION FOR SEQ ID NO:13:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 660 amino acids	
	(B) TYPE: amino acid	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(iii) HYPOTHETICAL: NO	
25	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)</pre>	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
	Met Arg Pro Arg Pro Ile Leu Leu Leu Leu Met Phe Leu Pro Met 1 5 10 15	
35	Leu Pro Ala Pro Pro Pro Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg 20 25 30	
	Arg Ser Gly Gly Ser Gly Gly Phe Trp Gly Asp Arg Val Asp Ser	
40	Gln Pro Phe Ala Ile Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Pro	

5	Asp 65	Val	Thr	Ala	Ala	Ala 70	Gly	Ala	Gly	Pro	Arg 75	Val	Arg	Gln	Pro	Ala 80
	Arg	Pro	Leu	Gly	Ser 85	Ala	Trp	Arg	Asp	Gln 90	Ala	Gln	Arg	Pro	Ala 95	Val
10	Ala	Ser	Arg	Arg 100	Arg	Pro	Thr	Thr	Ala 105	Gly	Ala	Ala	Pro	Leu 110	Thr	Ala
	Val	Ala	Pro 115	Ala	His	Asp	Thr	Pro 120	Pro	Val	Pro	Asp	Val 125	Asp	Ser	Arg
15	Gly	Ala 130	Ile	Leu	Arg	Arg	Gln 135	Tyr	Asn	Leu	Ser	Thr 140	Ser	Pro	Leu	Thr
20	Ser 145	Ser	Val	Ala	Thr	Gly 150	Thr	Asn	Leu	Val	Leu 155	Tyr	Ala	Ala	Pro	Leu 160
	Ser	Pro	Leu	Leu	Pro 165	Leu	Gln	Asp	Gly	Thr 170	Asn	Thr	His	Ile	Met 175	Ala
25	Thr	Glu	Ala	Ser 180	Asn	Tyr	Ala	Gln	Tyr 185	Arg	Val	Ala	Arg	Ala 190	Thr	Ile
	Arg	Tyr	Arg 195	Pro	Leu	Val	Pro	Asn 200	Ala	Val	Gly	Gly	Tyr 205	Ala	Ile	Ser
30	Ile	Ser 210	Phe	Trp	Pro	Gln	Thr 215	Thr	Thr	Thr	Pro	Thr 220	Ser	Val	Asp	Met
35	Asn 225	Ser	Ile	Thr	Ser	Thr 230	Asp	Val	Arg	Ile	Leu 235	Val	Gln	Pro	Gly	Ile 240
	Ala	Ser	Glu		Val 245	Ile	Pro	Ser	Glu	Arg 250	Leu	His	Tyr	Arg	Asn 255	Gln
40	Gly	Trp	Arg	Ser 260	Val	Glu	Thr	Ser	Gly 265	Val	Ala	Glu		Glu 270	Ala	Thr

	Ser G	ly Leu 275	Val	Met	Leu	Суз	Ile 280	His	Gly	Ser	Leu	Val 285	Asn	Ser	Tyr
5		sn Thr 90	Pro	Tyr	Thr	Gly 295	Ala	Leu	Gly	Leu	Leu 300	Asp	Phe	Ala	Leu
	Glu Lo	eu Glu	Phe	Arg	Asn 310	Leu	Thr	Pro	Gly	Asn 315	Thr	Asn	Thr	Arg	Val 320
10	Ser A	rg Tyr	Ser	Ser 325	Thr	Ala	Arg	His	Arg 330	Leu	Arg	Arg	Gly	Ala 335	Asp
15	Gly T	hr Ala	Glu 340	Leu	Thr	Thr	Thr	Ala 345	Ala	Thr	Arg	Phe	Met 350	Lys	Asp
	Leu T	yr Phe 355	Thr	Ser	Thr	Asn	Gly 360	Val	Gly	Glu	Ile	Gly 365	Arg	Gly	Ile
20		eu Thr 70	Leu	Phe	Asn	Leu 375	Ala	Asp	Thr	Leu	Leu 380	Gly	Gly	Leu	Pro
	Thr G	lu Leu	Ile	Ser	Ser 390	Ala	Gly	Gly	Gln	Leu 395	Phe	Tyr	Ser	Arg	Pro 400
25	Val V	al Ser	Ala	Asn 405	Gly	Glu	Pro	Thr	Val 410	ГÀа	Leu	Tyr	Thr	Ser 415	Val
30	Glu A	sn Ala	Gln 420	Gln	Asp	Lys	Gly	Ile 425	Ala	Ile	Pro	His	Asp 430	Ile	Asp
	Leu G	ly Glu 435	Ser	Arg	Val	Val	Ile 440	Gln	Asp	Tyr	Asp	Asn 445	Gln	His	Glu
35		sp Arg 50	Pro	Thr	Pro	Ser 455	Pro	Ala	Pro	Ser	Arg 460	Pro	Phe	Ser	Val
	Leu A:	rg Ala	Asn	Asp	Val 470	Leu	Trp	Leu	Ser	Leu 475	Thr	Ala	Ala	Glu	Tyr 480
40	Asp G	ln Ser	Thr	Tyr 485	Gly	Ser	Ser	Thr	Gly 490	Pro	Val	Tyr	Val	Ser 495	Asp

	Se	r Val	. Thr	Leu 500	Val	Asn	Val	Ala	Thr 505	Gly	Ala	Gln	Ala	Val 510	Ala	Arg
5	Se	r Leu	Asp 515	Trp	Thr	Lys	Val	Thr 520	Leu	Asp	Gly	Arg	Pro 525	Leu	Ser	Thr
	Il	e Gln 530		Tyr	Ser	Lys	Thr 535	Phe	Phe	Val	Leu	Pro 540	Leu	Arg	Gly	Lys
10	Le 54	u Ser 5	Phe	Trp	Glu	Ala 550	Gly	Thr	Thr	Lys	Ala 555	Gly	Tyr	Pro	Tyr	Asn 560
15	ту	r Asn	Thr	Thr	Ala 565	Ser	Asp	Gln	Leu	Leu 570	Val	Glu	Asn	Ala	Ala 575	Gly
	Hi	s Arg	Val	Ala 580	Ile	Ser	Thr	Tyr	Thr 585	Thr	Ser	Leu	Gly	Ala 590	Gly	Pro
20	Va	l Ser	Ile 595	Ser	Ala	Val	Ala	Val 600	Leu	Ala	Pro	His	Ser 605	Ala	Leu	Ala
	Le	u Leu 610		Asp	Thr	Leu	Asp 615	Tyr	Pro	Ala	Arg	Ala 620	His	Thr	Phe	Asp
25	As 62	p Phe	Cys	Pro	Glu	Сув 630	Arg	Pro	Leu	Gly	Leu 635	Gln	Gly	Cys	Ala	Phe 640
30	G1	n Ser	Thr	Val	Ala 645	Glu	Leu	Gln	Arg	Leu 650	Lys	Met	Lys	Val	Gly 655	Lys
	Th.	r Arg	Glu	Leu 660												
35	(2) INF	ORMAT	ION I	FOR S	SEQ I	ID NO	0:14:	:								
	(i	(B	UENCI) LEI) TYI) TOI	NGTH:	: 660 amino) ami	ino a		5							
40	(ii) MOL	ECULI	E TYE	?E: p	prote	ein									

(iii) HYPOTHETICAL: NO

(vi)	ORIGINAL	SOURCE:
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(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)
ORF-2

	(xi)	SEQ	JENCE	E DES	CRI	PTIO	V: SI	II QE	NO:	:14:						
	Met	Arg	Pro	Arg	Pro	Leu	Leu	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Pro	Met
10	1				5					10					15	
	Leu	Pro	Ala	Pro 20	Pro	Thr	Gly	Gln	Pro 25	Ser	Gly	Arg	Arg	Arg 30	Gly	Arc
15	Arg	Ser	Gly 35	Gly	Thr	Gly	Gly	Gly 40	Phe	Trp	Gly	Asp	Arg 45	Val	Asp	Ser
20	Gln	Pro 50	Phe	Ala	Ile	Pro	Tyr 55	Ile	His	Pro	Thr	Asn 60	Pro	Phe	Ala	Pro
	Asp 65	Val	Ala	Ala	Ala	Ser 70	Gly	Ser	Gly	Pro	Arg 75	Leu	Arg	Gln	Pro	Ala 80
25	Arg	Pro	Leu	Gly	Ser 85	Thr	Trp	Arg	Asp	Gln 90	Ala	Gln	Arg	Pro	ser 95	Ala
	Ala	Ser	Arg	Arg 100	Arg	Pro	Ala	Thr	Ala 105	Gly	Ala	Ala	Ala	Leu 110	Thr	Ala
30	Val	Ala	Pro 115	Ala	His	Asp	Thr	Ser 120	Pro	Val	Pro	Asp	Val 125	Asp	Ser	Arg
35	Gly	Ala 130	Ile	Leu	Arg	Arg	Gln 135	Tyr	Asn	Leu	Ser	Thr 140	Ser	Pro	Leu	Thr
	Ser 145	Ser	Val	Ala	Ser	Gly 150	Thr	Asn	Leu	Val	Leu 155	Tyr	Ala	Ala	Pro	Leu 160
40	Asn	Pro	Pro	Leu	Pro 165	Leu	Gln	Asp	Gly	Thr 170	Asn	Thr	His	Ile	Met 175	Ala

	Thr	Glu	Ala	Ser 180	Asn	Tyr	Ala	Gln	Tyr 185	Arg	Val	Ala	Arg	Ala 190	Thr	Ile
5	Arg	Tyr	Arg 195	Pro	Leu	Val	Pro	Asn 200	Ala	Val	Gly	Gly	Tyr 205	Ala	Ile	Ser
	Ile	Ser 210	Phe	Trp	Pro	Gln	Thr 215	Thr	Thr	Thr	Pro	Thr 220	Ser	Val	Asp	Met
10	Asn 225	Ser	Ile	Thr	Ser	Thr 230	Asp	Val	Arg	Ile	Leu 235	Val	Gln	Pro	Gly	11e 240
15	Ala	Ser	Glu	Leu	Val 245	Ile	Pro	Ser	Glu	Arg 250	Leu	His	Tyr	Arg	Asn 255	Gln
	Gly	Trp	Arg	ser 260	Val	Glu	Thr	Ser	Gly 265	Val	Ala	Glu	Glu	Glu 270	Ala	Thr
20	Ser	Gly	Leu 275	Val	Met	Leu	Cys	Ile 280	His	Gly	Ser	Pro	Val 285	Asn	Ser	Tyr
	Thr	Asn 290	Thr	Pro	Tyr	Thr	Gly 295	Ala	Leu	Gly	Leu	Leu 300	Asp	Phe	Ala	Leu
25	Glu 305	Leu	Glu	Phe	Arg	Asn 310	Leu	Thr	Thr	Суз	Asn 315	Thr	Asn	Thr	Arg	Val 320
30	Ser	Arg	Tyr	Ser	Ser 325	Thr	Ala	Arg	His	Arg 330	Leu	Arg	Arg	Gly	Ala 335	Asp
	Gly	Thr	Ala	Glu 340	Leu	Thr	Thr	Thr	Ala 345	Ala	Thr	Arg	Phe	Met 350	Lys	Asp
35	Leu	His	Phe 355	Thr	Gly	Leu	Asn	Gly 360	Val	Gly	Glu	Val	Gly 365	Arg	Gly	Ile
	Ala	Leu 370	Thr	Leu	Leu	Asn	Leu 375	Ala	Asp	Thr	Leu	Leu 380	Gly	Gly	Leu	Pro
40	Thr 385	Glu	Leu	Ile	Ser	Ser 390	Ala	Glү	Gly	Gln	Leu 395	Phe	Tyr	Ser	Arg	Pro 400

		Val			405					410					415	
, 5	Glu	Asn A		31n 420	Gln	Asp	Lys	Gly	Val 425	Ala	Ile	Pro	His	Asp 430	Ile	Asp
	Leu	Gly A	Asp 8 435	Ser .	Arg	Val	Val	Ile 440	Gln	Asp	Tyr	Asp	Asn 445	Gln	His	Glu
10	Gln	Asp 1	Arg E	Pro '	Thr	Pro	Ser 455	Pro	Ala	Pro	Ser	Arg 460	Pro	Phe	Ser	Val
15	Leu 465	Arg A	Ala A	Asn i	Asp	Val 470	Leu	Trp	Leu	Ser	Leu 475	Thr	Ala	Ala	Glu	Tyr 480
	Asp	Gln S	Ser I		Tyr 485	Gly	Ser	Ser	Thr	Gly 490	Pro	Val	Tyr	Ile	Ser 495	Asp
20	Ser	Val 1		eu 1	Val	Asn	Val	Ala	Thr 505	Gly	Ala	Gln	Ala	Val 510	Ala	Arg
	Ser	Leu A	Asp T	rp s	Ser	Lys	Val	Thr 520	Leu	Asp	Gly	Arg	Pro 525	Leu	Pro	Thr
25	Val	Glu 0	Gln T	Yr s	Ser	Lys	Thr 535	Phe	Phe	Val	Leu	Pro 540	Leu	Arg	Gly	Lys
30	Leu 545	Ser F	Phe T	rp (Ala 550	Gly	Thr	Thr	Lys	Ala 555	Gly	Tyr	Pro	Tyr	Asn 560
	Tyr	Asn T	Thr T		Ala 565	Ser	Asp	Gln	Ile	Leu 570	Ile	Glu	Asn	Ala	Ala 575	Gly
35	His	Arg V		la 1 80	Ile	Ser	Thr	Tyr	Thr 585	Thr	Arg	Leu	Gly	Ala 590	Gly	Pro
	Val	Ala I	[le S	er A	Ala	Ala		Val 600	Leu	Ala	Pro	Arg	Ser 605	Ala	Leu	Ala
40	Leu	Leu G 610	3lu A	.sp T	Chr		Asp 615	Tyr	Pro	Gly		Ala 620	His	Thr	Phe	Asp

	Asp 625	Phe	Cys	Pro	Glu	630 Cys	Arg	Ala	Leu	Gly	Leu 635	Gln	Gly	Сув	Ala	Phe 640
5	Gln	Ser	Thr	Val	Ala 645	Glu	Leu	Gln	Arg	Leu 650	Lys	Val	Lys	Val	Gly 655	Lys
	Thr	Arg	Glu	Leu 660												
10	(2) INFO	RMAT:	ION 1	FOR :	SEQ :	ID N	0:15	:								
15	(i)	(B) LEI) TYI	NGTH	ARAC: 549 amino	9 am:	ino a	acid	s							
					GY:		_									
	(ii)	MOLI	ECULI	E TY	PE:]	prote	ein									
20	(iii)	НҮРС	OTHE?	ricai	L: NO)										
25	(vi)			IIVI	URCE: DUAL kDa,	ISO			pati	tis I	E vi i	cus	(Bur	ma si	trai	1)
	(xi)	SEQ	JENCI	E DES	SCRII	PTIOI	N: SI	EQ II	ом о	:15:						
30	Ala 1	Val	Ala	Pro	Ala 5	His	Asp	Thr	Pro	Pro 10	Val	Pro	Asp	Val	Asp 15	Ser
	Arg	Gly	Ala	Ile 20	Leu	Arg	Arg	Gln	Tyr 25	Asn	Leu	Ser	Thr	ser 30	Pro	Leu
35	Thr	Ser	Ser 35	Val	Ala	Thr	Gly	Thr 40	Asn	Leu	Val	Leu	Tyr 45	.Ala	Ala	Pro
	Leu	Ser 50	Pro	Leu	Leu	Pro	Leu 55	Gln	Asp	Gly	Thr	Asn 60	Thr	His	Ile	Met
40	Ala	Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Ala	Arg	Ala	Thr

	Pro Val 7	Val Ser Al	a Asn Gly 295		hr Val Lys 300	Leu Tyr Thr Se	er
5	Val Glu 2	Asn Ala Gl	n Gln Asp 310	Lys Gly I	le Ala Ile 315	Pro His Asp I	le 20
	Asp Leu (Gly Glu Se 32	•		In Asp Tyr 30	Asp Asn Gln H	is
10	Glu Gln 7	Asp Arg Pr 340	o Thr Pro	Ser Pro A 345	la Pro Ser	Arg Pro Phe Se	er
15		Arg Ala As 355	n Asp Val	. Leu Trp L 360	eu Ser Leu	Thr Ala Ala G	lu
	Tyr Asp (Gln Ser Th	r Tyr Gly 375		hr Gly Pro 380	Val Tyr Val Se	er
20	Asp Ser	Val Thr Le	u Val Asn 390	n Val Ala T	hr Gly Ala 395	Gln Ala Val Al	1a 00
	Arg Ser	Leu Asp Tr 40			eu Asp Gly	Arg Pro Leu Se 415	er
25	Thr Ile	Gln Gln Ty 420	r Ser Lys	Thr Phe P 425	he Val Leu	Pro Leu Arg Gl	ly
30		435		440	-	Gly Tyr Pro Ty 445	-
	450		455	5	460	Glu Asn Ala A	
35	Gly His .	Arg Val Al	a Ile Ser 470	Thr Tyr T	hr Thr Ser 475	Leu Gly Ala G	ly 80
	Pro Val	Ser Ile Se 48			eu Ala Pro 90	His Ser Ala Le 495	eu
40	Ala Leu	Leu Glu As 500	p Thr Leu	Asp Tyr P 505	ro Ala Arg	Ala His Thr Pl	he

	Asp	Asp	Phe 515	Суз	Pro	Glu	Суз	Arg 520	Pro	Leu	Gly	Leu	Gln 525	Gly	Суз	Ala
5	Phe	Gln 530	Ser	Thr	Val	Ala	Glu 535	Leu	Gln	Arg	Leu	Lys 540	Met	Lys	Val	Gly
	Lys 545	Thr	Arg	Glu	Leu											
10	(2) INFOR	TAM	ON E	FOR S	SEQ I	ID NO	16:	:								
15	(i)	(B)	LEN TYI STI	NGTH: PE: & RANDI	: 549 amino EDNES	e ami	ino a id singl	acids	3							
		(D)	TOE	SOTO	3Y: 1	linea	ar									
	(ii)	MOLE	ECULI	E TYP	?E: 1	prote	ein									
20	(iii)	НҮРС	THE	ricai	C: NO	ס										
	(vi)			IVIC	UAL				patit	tis I	E vi:	rus	(Mex	ico s	strai	in)
25																
	(xi)	SEQU	JENCI	E DES	CRII	PTIO	N: SI	EQ II	ONO:	:16:						
30	Ala 1	Val	Ala	Pro	Ala 5	His	Asp	Thr	Ser	Pro 10	Val	Pro	Asp	Val	Asp 15	Ser
	Arg	Gly	Ala	Ile 20	Leu	Arg	Arg	Gln	Tyr 25	Asn	Leu	Ser	Thr	Ser 30	Pro	Leu
35	Thr	Ser	Ser 35	Val	Ala	Ser	Gly	Thr 40	Asn	Leu	Val	Leu	Tyr 45	Ala	Ala	Pro
40	Leu	Asn 50	Pro	Pro	Leu	Pro	Leu 55	Gln	Asp	Gly	Thr	Asn 60	Thr	His	Ile	Met
	Ala	Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Ala	Arg	Ala	Thr

	Pro	Val 290		Ser	Ala	Asn	Gly 295		Pro	Thr	Val	100 Lys	Leu	Tyr	Thr	Ser
5	Val 305	Glu	Asn	Ala	Gln	Gln 310	Asp	ГÀа	Gly	Val	Ala 315	Ile	Pro	His	Asp	Ile 320
	Asp	Leu	Gly	Asp	Ser 325	Arg	Val	Val	Ile	Gln 330	Asp	Tyr	Asp	Asn	Gln 335	His
10	Glu	Gln	Asp	Arg 340	Pro	Thr	Pro	Ser	Pro 345	Ala	Pro	Ser	Arg	Pro 350	Phe	Ser
15	Val	Leu	Arg 355	Ala	Asn	Asp	Val	Leu 360	Trp	Leu	Ser	Leu	Thr 365	Ala	Ala	Glu
	Tyr	Asp 370	Gln	Ser	Thr	Tyr	Gly 375	Ser	Ser	Thr	Gly	Pro 380	Val	Tyr	Ile	Ser
20	As p 385	Ser	Val	Thr	Leu	Val 390	Asn	Val	Ala	Thr	Gly 395	Ala	Gln	Ala	Val	Ala 400
	Arg	Ser	Leu	Asp	Trp 405	Ser	Lys	Val	Thr	Leu 410	Asp	Gly	Arg	Pro	Leu 415	Pro
25	Thr	Val	Glu	Gln 420	Tyr	Ser	Lys	Thr	Phe 425	Phe	Val	Leu	Pro	Leu 430	Arg	Gly
30	Lys	Leu	Ser 435	Phe	Trp	Glu	Ala	Gly 440	Thr	Thr	Lys	Ala	Gly 445	Tyr	Pro	Tyr
	Asn	Tyr 450	Asn	Thr	Thr	Ala	Ser 455	Asp	Gln	Ile	Leu	Ile 460	Glu	Asn	Ala	Ala
35	Gly 465	His	Arg	Val	Ala	Ile 470	Ser	Thr	Tyr	Thr	Thr 475	Arg	Leu	Gly	Ala	Gly 480
	Pro	Val	Ala	Ile	Ser 485	Ala	Ala	Ala		Leu 490	Ala	Pro	Arg	Ser	Ala 495	Leu
40	Ala	Leu	Leu	Glu 500	Asp	Thr	Phe	Asp	Tyr 505	Pro	Gly	Arg	Ala	His 510	Thr	Phe

Asp Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala

			515					520					525			
5	Phe	Gln 530	Ser	Thr	Val	Ala	Glu 535	Leu	Gln	Arg	Leu	Lys 540	Val	Lys	Val	Gly
	Lys 545	Thr	Arg	Glu	Leu											
10	(2) INFO	TAMS	ON E	FOR S	SEQ :	ID NO	D:17	:								
15	(i)	(B)	LEN TYP	NGTH:	: 32 [°] amino	reria 7 am: 5 ac: linea	ino a Ld		3							
	(ii)	MOLE	CULE	TY!	PE: J	prote	ein									
20	(iii)	НҮРС	THE	FICAI	L: NO)										
20	(vi)				DUAL		LATE :	: Her	patit	tis I	E Vi	cus	(Buri	ma st	crain	n) SG3
25																
	(xi)	SEQU	IENCE	E DES	SCRII	PTIO	N: SI	EQ II	O NO:	:17:						
	Gly 1	Ala	Asp	Gly	Thr 5	Ala	Glu	Leu	Thr	Thr 10	Thr	Ala	Ala	Thr	Arg 15	Phe
30	Met	Lys	Asp	Leu 20	Tyr	Phe	Thr	Ser	Thr 25	Asn	Gly	Val	Gly	Glu 30	Ile	Gly
35	Arg	Gly	Ile 35	Ala	Leu	Thr	Leu	Phe 40	Asn	Leu	Ala	Asp	Thr 45	Leu	Leu	Gly
	Gly	Leu 50	Pro	Thr	Glu	Leu	Ile 55	Ser	Ser	Ala	Gly	Gly 60	Gln	Leu	Phe	Tyr
40	Ser 65	Arg	Pro	Val	Val	ser 70	Ala	Asn	Gly	Glu	Pro 75	Thr	Val	Lys	Leu	Tyr 80

	Thr Ser	Val Glu	Asn Ala 85	Gln Glr	Asp Lys	s Gly Ile	Ala Ile	Pro His 95
5	Asp Ile	Asp Leu 100	Gly Glu	Ser Aro	Val Val	l Ile Gln	Asp Tyr 110	Asp Asn
	Gln His	Glu Gln 115	Asp Arg	Pro Thr		r Pro Ala	Pro Ser 125	Arg Pro
10	Phe Ser		Arg Ala	Asn Asp	Val Le	u Trp Leu 140	Ser Leu	Thr Ala
15	Ala Glu 145	Tyr Asp	Gln Ser 150	Thr Tyr	Gly Ser	r Ser Thr 155	Gly Pro	Val Tyr 160
	Val Ser	Asp Ser	Val Thr 165	Leu Val	. Asn Val	l Ala Thr	Gly Ala	Gln Ala 175
20	Val Ala	Arg Ser 180	Leu Asp	Trp Thr	Lys Val	l Thr Leu	Asp Gly 190	Arg Pro
	Leu Ser	Thr Ile	Gln Gln	Tyr Ser	=	r Phe Phe	Val Leu 205	Pro Leu
25	Arg Gly 210		Ser Phe	Trp Glu 215	Ala Gly	y Thr Thr 220	Lys Ala	Gly Tyr
30	Pro Tyr 225	Asn Tyr	Asn Thr 230	Thr Ala	Ser Ası	p Gln Leu 235	Leu Val	Glu Asn 240
	Ala Ala	Gly His	Arg Val 245	Ala Ile	Ser Thi	r Tyr Thr	Thr Ser	Leu Gly 255
35	Ala Gly	Pro Val 260	Ser Ile	Ser Ala	Val Ala 265	a Val Leu	Ala Pro 270	His Ser
	Ala Leu	Ala Leu 275	Leu Glu	Asp Thr	-	p Tyr Pro	Ala Arg 285	Ala His
40	Thr Phe		Phe Cys	Pro Glu 295	ı Cys Arq	g Pro Leu 300	Gly Leu	Gln Gly

Cys Ala Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Met Lys

Val Gly Lys Thr Arg Glu Leu (2) INFORMATION FOR SEQ ID NO:18: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO (vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain) SG3 region (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His

	Asp	lle	Asp	Leu 100	Gly	Asp	Ser	Arg	Val 105		Ile	Gln	Asp	туг 110	Asp	Asn
5	Gln	His	Glu 115	Gln	Asp	Arg	Pro	Thr 120	Pro	Ser	Pro	Ala	Pro 125	Ser	Arg	Pro
	Phe	Ser 130		Leu	Arg	Ala	Asn 135	Asp	Val	Leu	Trp	Leu 140	Ser	Leu	Thr	Ala
10	Ala 145	Glu	Tyr	Asp	Gln	Ser 150	Thr	Tyr	Gly	Ser	Ser 155	Thr	Gly	Pro	Val	Tyr 160
15	Ile	Ser	Asp	Ser	Val 165	Thr	Leu	Val	Asn	Val 170	Ala	Thr	Gly	Ala	Gln 175	Ala
	Val	Ala	Arg	Ser 180	Leu	Asp	Trp	Ser	Lys 185	Val	Thr	Leu	Asp	Gly 190	Arg	Pro
20	Leu	Pro	Thr 195	Val	Glu	Gln	Tyr	Ser 200	Lys	Thr	Phe	Phe	Val 205	Leu	Pro	Leu
	Arg	Gly 210	Lys	Leu	Ser	Phe	Trp 215	Glu	Ala	Gly	Thr	Thr 220	Lys	Ala	Gly	Tyr
25	Pro 225	Tyr	Asn	Tyr	Asn	Thr 230	Thr	Ala	Ser	Asp	Gln 235	Ile	Leu	Ile	Glu	Asn 240
30	Ala	Ala	Gly	His	Arg 245	Val	Ala	Ile	Ser	Thr 250	Tyr	Thr	Thr	Arg	Leu 255	Gly
	Ala	Gly	Pro	Val 260	Ala	Ile	Ser	Ala	Ala 265	Ala	Val	Leu	Ala	Pro 270	Arg	Ser
35	Ala	Leu	Ala 275	Leu	Leu	Glu	Asp	Thr 280	Phe	Asp	Tyr	Pro	Gly 285	Arg	Ala	His
	Thr	Phe 290	Asp	Asp	Phe	Cys	Pro 295	Glu	Cys	Arg	Ala	Leu 300	Gly	Leu	Gln	Gly
40	Сув 305	Ala	Phe	Gln	Ser	Thr 310	Val	Ala	Glu	Leu	Gln 315	Arg	Leu	ГЛЗ	Val	Lys 320

Val Gly Lys Thr Arg Glu Leu 325

(iii) HYPOTHETICAL: NO

5	(2) INFORMATION FOR SEQ ID NO:19:
j	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
10	
	(ii) MOLECULE TYPE: protein
	(iii) HYPOTHETICAL: NO
15	(vi) ORIGINAL SOURCE:
	(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
	406.4-2
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
	(NI) OBSOLAGE PEROKITION. BEST IN NO.13.
	Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro Ser
	1 5 10 15
2.5	
25	Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly Pro Arg 20 25 30
	20 25 30
	Arg
30	
	(2) INFORMATION FOR SEQ ID NO:20:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 33 amino acids
35	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
	(11) Mondood III. process

	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)</pre>													
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:													
10	Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser 1 5 10 15													
	Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg 20 25 30													
15	Arg													
	(2) INFORMATION FOR SEQ ID NO:21:													
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 124 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear													
25	(ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO													
30	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma Strain)</pre>													
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:													
35	Met Asn Asn Met Ser Phe Ala Ala Pro Met Gly Ser Arg Pro Cys Ala 1 5 10 15													
	Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro 20 25 30													
40	Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly Ala Ala													

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	Arg	His Arg	g Pro	Val	Ser	Arg	Leu 40	Ala	Ala	Val	Val	Gly 45	Gly	Ala	Ala
5	Ala	Val Pro	Ala	Val	Val	Ser 55	Gly	Val	Thr	Gly	Leu 60	Ile	Leu	Ser	Pro
	Ser 65	Gln Ser	Pro	Ile	Phe 70	Ile	Gln	Pro	Thr	Pro 75	Leu	Pro	Gln	Thr	Leu 80
10	Pro	Leu Arg	, Pro	Gly 85	Leu	Asp	Leu	Ala	Phe 90	Ala	Asn	Gln	Pro	Gly 95	His
15	Leu	Ala Pro	100	Gly	Glu	Ile	Arg	Pro 105	Ser	Ala	Pro	Pro	Leu 110	Pro	Pro
	Val	Ala Asp		Pro	Gln	Pro	Gly 120	Leu	Arg	Arg	Glx				
20	(2) INFORMATION FOR SEQ ID NO:23:														
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 48 amino acids(B) TYPE: amino acid														
25		(D) TC	POLOG	Y:]	Linea	ır									
	(ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO														
30	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)</pre>														
35	(xi)	SEQUENC	E DES	CRIE	NOIT	I: SE	Q II) NO:	23:						
	Thr 1	Leu Asp	Tyr	Pro 5	Ala	Arg	Ala	His	Thr 10	Phe	Asp	Asp	Phe	Cys 15	Pro
40	Glu	Cys Arg	Pro 20	Leu	Gly	Leu	Gln	Gly 25	Cys	Ala	Phe	Gln	ser 30	Thr	Val

Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Leu

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5 (2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 amino acids (B) TYPE: amino acid 10 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (iii) HYPOTHETICAL: NO 15 (vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain) 406.3-2 region 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe Asp Asp Phe Cys Pro 1 5 10 15 25 Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val 20 25 30 Ala Glu Leu Gln Arg Leu Lys Val Lys Val Gly Lys Thr Arg Glu Leu 30 40 45 (2) INFORMATION FOR SEQ ID NO:25: (i) SEQUENCE CHARACTERISTICS: 35 (A) LENGTH: 540 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain) r62kDa, 58.1 kDa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

10 Ala Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser
1 5 10 15

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu 20 25 30

15

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Thr Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro 35 40 45

Leu Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met 50 55 60

Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr 65 70 75 80

25 Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile 85 90 95

Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp
100 105 110

Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly
115 120 125

Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn 130 135 140

Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala 145 150 155 160

40 Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Leu Val Asn Ser 165 170 175

	Tyr 1	Thr Asn	Thr 180	Pro	Tyr	Thr	Gly	Ala 185	Leu	Gly	Leu	Leu	Asp 190	Phe	Ala
5	Leu G	Slu Leu 195		Phe	Arg	Asn	Leu 200	Thr	Pro	Gly	Asn	Thr 205	Asn	Thr	Arg
		Ser Arg 210	Tyr	Ser	Ser	Thr 215	Ala	Arg	His	Arg	Leu 220	Arg	Arg	Gly	Ala
10	Asp G 225	ly Thr	Ala	Glu	Leu 230	Thr	Thr	Thr	Ala	Ala 235	Thr	Arg	Phe	Met	Lys 240
15	Asp I	Leu Tyr	Phe	Thr 245	Ser	Thr	Asn	Gly	Val 250	Gly	Glu	Ile	Gly	Arg 255	Gly
	Ile A	Ala Leu	Thr 260	Leu	Phe	Asn	Leu	Ala 265	Asp	Thr	Leu	Leu	Gly 270	Gly	Leu
20	Pro I	Thr Glu 275		Ile	Ser	Ser	Ala 280	Gly	Gly	Gln	Leu	Phe 285	Tyr	Ser	Arg
		/al Val 290	Ser	Ala	Asn	Gly 295	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser
25	Val 6	Glu Asn	Ala	Gln	Gln 310	Asp	Lys	Gly	Ile	Ala 315	Ile	Pro	His	Asp	Ile 320
30	Asp I	Leu Gly	Glu	Ser 325	Arg	Val	Val	Ile	Gln 330	Asp	Tyr	Asp	Asn	Gln 335	His
	Glu G	Gln Asp	Arg 340	Pro	Thr	Pro	Ser	Pro 345	Ala	Pro	Ser	Arg	Pro 350	Phe	Ser
35	Val I	Leu Arg		Asn	Asp	Val	Leu 360	Trp	Leu	Ser	Leu	Thr 365	Ala	Ala	Glu
	-	Asp Glr 370	Ser	Thr	Tyr	Gly 375	Ser	Ser	Thr	Gly	Pro 380	Val	Tyr	Val	Ser
40	Asp S	Ser Val	Thr	Leu	Val 390	Asn	Val	Ala	Thr	Gly 395	Ala	Gln	Ala	Val	Ala 400

	Arg	Ser	Leu	Asp	Trp 405	Thr	Lys	Val	Thr	Leu 410	Asp	Gly	Arg	Pro	Leu 415	Ser
5	Thr	Ile	Gln	Gln 420	Tyr	Ser	Lys	Thr	Phe 425	Phe	Val	Leu	Pro	Leu 430	Arg	Gly
	Lys	Leu	Ser 435	Phe	Trp	Glu	Ala	Gly 440	Thr	Thr	ГЛа	Ala	Gly 445	Tyr	Pro	Tyr
10	Asn	Tyr 450	Asn	Thr	Thr	Ala	Ser 455	Asp	Gln	Leu	Leu	Val 460	Glu	Asn	Ala	Ala
15	Gly 465		Arg	Val	Ala	Ile 470	Ser	Thr	Tyr	Thr	Thr 475	Ser	Leu	Gly	Ala	Gly 480
	Pro	Val	Ser	Ile	Ser 485	Ala	Val	Ala	Val	Leu 490	Ala	Pro	His	Ser	Ala 495	Leu
20	Ala	Leu	Leu	Glu 500	Asp	Thr	Leu	Asp	Tyr 505	Pro	Ala	Arg	Ala	His 510	Thr	Phe
	Asp	Asp	Phe 515	Cys	Pro	Glu	Суз	Arg 520	Pro	Leu	Gly	Leu	Gln 525	Gly	Cys	Ala
25	Phe	Gln 530		Thr	Val	Ala	Glu 535	Leu	Gln	Arg	Leu	Lys 540				
	(2) INFO	RMATI	ON F	OR S	SEQ I	D NC	26:									
30	(i)	(A)	LEN TYP	GTH:	ARACT 540 umino	ami aci	.no a .d	cids	3							
35		(D)	TOP	OLOG	Y: 1	inea	ır									
	(ii)	MOLE	CULE	TYP	E: p	rote	in									
	(iii)	нүрс	THET	'ICAL	: NO	٠										
40	(vi)				RCE:	ISOL	ATE:	Нер	atit	is E	vir	us (Mexi	co s	trai	n)

r62kDa, 58.1 kDa

	(xi)	SEQ	JENCI	E DES	SCRII	PTIO	1: SI	EQ II	ONO:	:26:						
5	Ala 1	Val	Ala	Pro	Ala 5	His	Asp	Thr	Ser	Pro 10	Val	Pro	Asp	Val	Asp 15	Ser
10	Arg	Gly	Ala	Ile 20	Leu	Arg	Arg	Gln	Tyr 25	Asn	Leu	Ser	Thr	Ser 30	Pro	Leu
	Thr	Ser	Ser 35	Val	Ala	Ser	Gly	Thr 40	Asn	Leu	Val	Leu	Tyr 45	Ala	Ala	Pro
15	Leu	Asn 50	Pro	Pro	Leu	Pro	Leu 55	Gln	Asp	Gly	Thr	Asn 60	Thr	His	Ile	Met
	Ala 65	Thr	Glu	Ala	Ser	Asn 70	Tyr	Ala	Gln	Tyr	Arg 75	Val	Ala	Arg	Ala	Thr 80
20	Ile	Arg	Tyr	Arg	Pro 85	Leu	Val	Pro	Asn	Ala 90	Val	Gly	Gly	Tyr	Ala 95	Ile
	Ser	Ile	Ser	Phe 100	Trp	Pro	Gln	Thr	Thr 105	Thr	Thr	Pro	Thr	Ser 110	Val	Asp
25	Met	Asn	Ser 115	Ile	Thr	Ser	Thr	Asp 120	Val	Arg	Ile	Leu	Val 125	Gln	Pro	Gly
30 .	Ile	Ala 130	Ser	Glu	Leu	Val	Ile 135	Pro	Ser	Glu	Arg	Leu 140	His	Tyr	Arg	Asn
	Gln 145	Gly	Trp	Arg	Ser	Val 150	Glu	Thr	Ser	Gly	Val 155	Ala	Glu	Glu	Glu	Ala 160
35	Thr	Ser	Gly	Leu	Val 165	Met	Leu	Cys	Ile	His 170	Gly	Ser	Pro	Val	Asn 175	Ser
	Tyr	Thr	Asn	Thr 180	Pro	Tyr	Thr	Gly	Ala 185	Leu	Gly	Leu	Leu	Asp 190	Phe	Ala
40	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Thr	Сув	Asn	Thr	Asn	Thr	Arg

Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Ile Ser Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala

Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Pro

	Thr	Vai	GIu	420	Tyr	Ser	råa	Thr	425	Pne	Val	Leu	Pro	430	Arg	GTÅ
5	Lys	Leu	Ser 435	Phe	Trp	Glu	Ala	Gly 440	Thr	Thr	Lys	Ala	Gly 445	Tyr	Pro	Tyr
	Asn	Tyr 450	Asn	Thr	Thr	Ala	Ser 455	Asp	Gln	Ile	Leu	Ile 460	Glu	Asn	Ala	Ala
10	Gly 465	His	Arg	Val	Ala	Ile 470	Ser	Thr	Tyr	Thr	Thr 475	Arg	Leu	Gly	Ala	Gly 480
15	Pro	Val	Ala	Ile	Ser 485	Ala	Ala	Ala	Val	Leu 490	Ala	Pro	Arg	Ser	Ala 495	Leu
	Ala	Leu	Leu	Glu 500	Asp	Thr	Phe	Asp	Tyr 505	Pro	Gly	Arg	Ala	His 510	Thr	Phe
20	Asp	Asp	Phe 515	Cys	Pro	Glu	Суз	Arg 520	Ala	Leu	Gly	Leu	Gln 525	Gly	Суз	Ala
	Phe	Gln 530	Ser	Thr	Val	Ala	Glu 535	Leu	Gln	Arg	Leu	Lys 540				
25	(2) INFO	RMATI	ON I	FOR S	SEQ I	ID NO	D:27:	:								
	(i)		LE	GTH:		5 am:	ino a	S: acids	3							
30		(C)	ST	RANDI	EDNES	ss: s	sing:	Le								
	(ii)	MOLE	CULI	E TYI	PE:]	prote	∍in									
35	(iii)	нүро	THE	ricai	L: NO	0										
	(vi)	ORIG		IVIC		ISO			patit	tis I	E vi	cus	(Burr	ma st	crain	1)
40																

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

5	Ala Val	Ala Pro 1	Ala His 5	Asp Thr	Pro Pro	Val Pro	Asp Val	Asp Ser 15
	Arg Gly	Ala Ile I 20	Leu Arg	Arg Gln	Tyr Asr	Leu Ser	Thr Ser	Pro Leu
10		Ser Val <i>I</i> 35	Ala Thr	Gly Thr 40	Asn Leu	Val Leu	Tyr Ala 45	Ala Pro
	Leu Ser 50	Pro Leu I	Leu Pro	Leu Gln 55	Asp Gly	Thr Asn	Thr His	Ile Met
15	Ala Thr	Glu Ala S	Ser Asn 70	Tyr Ala	Gln Tyr	Arg Val	Ala Arg	Ala Thr 80
20	Ile Arg	Tyr Arg E	Pro Leu 85	Val Pro	Asn Ala	Val Gly	Gly Tyr	Ala Ile 95
	Ser Ile	Ser Phe 1	Trp Pro	Gln Thr	Thr Thr	Thr Pro	Thr Ser	Val Asp
25	Met Asn	Ser Ile 1	Thr Ser	Thr Asp	Val Arg	Ile Leu	Val Gln 125	Pro Gly
	Ile Ala :	Ser Glu I		Ile Pro 135	Ser Glu	Arg Leu 140	His Tyr	Arg Asn
30	Gln Gly 1	Trp Arg S	Ser Val	Glu Thr	Ser Gly	Val Ala 155	Glu Glu	Glu Ala 160
35	Thr Ser (Val Met 165	Leu Cys	Ile His	Gly Ser	Leu Val	Asn Ser
	Tyr Thr	Asn Thr F	Pro Tyr	Thr Gly	Ala Leu 185	Gly Leu	Leu Asp	Phe Ala
40	Leu Glu I	Leu Glu P 195	Phe Arg	Asn Leu 200	Thr Pro	Gly Asn	Thr Asn 205	Thr Arg

	Val	Ser 210	Arg	Tyr	Ser	Ser	Thr 215	Ala	Arg	His	Arg	Leu 220	Arg	Arg	Gly	Ala
5	Asp 225	Gly	Thr	Ala	Glu	Leu 230	Thr	Thr	Thr	Ala	Ala 235	Thr	Arg	Phe	Met	Lys 240
	Asp	Leu	Tyr	Phe	Thr 245	Ser	Thr	Asn	Gly	Val 250	Gly	Glu	Ile	Gly	Arg 255	Gly
10	Ile	Ala	Leu	Thr 260	Leu	Phe	Asn	Leu	Ala 265	Asp	Thr	Leu	Leu	Gly 270	Gly	Leu
15	Pro	Thr	Glu 275	Leu	Ile	Ser	Ser	Ala 280	Gly	Gly	Gln	Leu	Phe 285	Tyr	Ser	Arg
	Pro	Val 290	Val	Ser	Ala	Asn	Gly 295	Glu	Pro	Thr	Val	Lys 300	Leu	Tyr	Thr	Ser
20	Val 305	Glu	Asn	Ala	Gln	Gln 310	Asp	Lys	Gly	Ile	Ala 315	Ile	Pro	His	Asp	Ile 320
	Asp	Leu	Gly	Glu	Ser 325	Arg	Val	Val	Ile	Gln 330	Asp	Tyr	Asp	Asn	Gln 335	His
25	Glu	Gln	Asp	Arg 340	Pro	Thr	Pro	Ser	Pro 345	Ala	Pro	Ser	Arg	Pro 350	Phe	Ser
30	Val	Leu	Arg 355	Ala	Asn	Asp	Val	Leu 360	Trp	Leu	Ser	Leu	Thr 365	Ala	Ala	Glu
	Tyr	Asp 370	Gln	Ser	Thr	Tyr	Gly 375	Ser	Ser	Thr	Gly	Pro 380	Val	Tyr	Val	Ser
35	Asp 385	Ser	Val	Thr	Leu	Val 390	Asn	Val	Ala	Thr	Gly 395	Ala	Gln	Ala	Val	Ala 400
	Arg	Ser	Leu		Trp 405	Thr	Lys	Val	Thr	Leu 410	Asp	Gly	Arg	Pro	Leu 415	Ser
40	Thr	Ile	Gln	Gln 420	Tyr	Ser	Lys	Thr	Phe 425	Phe	Val	Leu	Pro	Leu 430	Arg	Gly

	ГЛа	Leu	Ser 435	Phe	Trp	Glu	Ala	Gly 440	Thr	Thr	ГÀа	Ala	Gly 445	Tyr	Pro	Tyr
5	Asn	Tyr 450	Asn	Thr	Thr	Ala	Ser 455	Asp	Gln	Leu	Leu	Val 460	Glu	Asn	Ala	Ala
	Gly 465	His	Arg	Val	Ala	Ile 470	Ser	Thr	Tyr	Thr	Thr 475	Ser	Leu	Gly	Ala	Gly 480
10	Pro	Val	Ser	Ile	Ser 485	Ala	Val	Ala	Val	Leu 490	Ala	Pro	His	Ser	Ala 495	Leu
15	Ala	Leu	Leu	Glu 500	Asp	Thr	Leu	Asp	Tyr 505	Pro	Ala	Arg	Ala	His 510	Thr	Phe
15	Asp	Asp	Phe 515	Cys	Pro	Glu	Cys	Arg 520	Pro	Leu	Gly	Leu	Gln 525			
20	(2) INFO	RMATI	ON I	FOR S	SEQ :	ID N	o:28	:								
	(i)	, ,	LEI	NGTH	: 52		ino	S: acid	s							
25		• •				ss: line		le								
	(ii)	MOLI	ECUL	E TY	PE:	prot	ein									
30	(iii)	HYPO	OTHE'	TICA	L: N	0										
	(vi)	ORIO		DIVI	DUAL				pati	tis	E vi	rus	(Mex	ico	stra	in)
35																
		SEQI Val										Pro	Asp	Val	Asp 15	Ser
40	Arg	g Gly	Ala	Ile 20	Leu	Arg	Arg	Gln	Tyr 25	Asn	. Leu	Ser	Thr	Ser	Pro	Leu

	Thr	Ser	Ser 35	Val	Ala	Ser	Gly	Thr 40	Asn	Leu	Val	Leu	Tyr 45	Ala	Ala	Pro
5	Leu	Asn 50	Pro	Pro	Leu	Pro	Leu 55	Gln	Asp	Gly	Thr	Asn 60	Thr	His	Ile	Met
	Ala 65	Thr	Glu	Ala	Ser	Asn 70	Tyr	Ala	Gln	Tyr	Arg 75	Val	Ala	Arg	Ala	Thr 80
10	Ile	Arg	Tyr	Arg	Pro 85	Leu	Val	Pro	Asn	Ala 90	Val	Gly	Gly	Tyr	Ala 95	Ile
15	Ser	Ile	Ser	Phe 100	Trp	Pro	Gln	Thr	Thr 105	Thr	Thr	Pro	Thr	Ser 110	Val	Asp
	Met	Asn	Ser 115	Ile	Thr	Ser	Thr	Asp 120	Val	Arg	Ile	Leu	Val 125	Gln	Pro	Gly
20	Ile	Ala 130	Ser	Glu	Leu	Val	Ile 135	Pro	Ser	Glu	Arg	Leu 140	His	Tyr	Arg	Asn
	Gln 145	Gly	Trp	Arg	Ser	Val 150	Glu	Thr	Ser	Gly	Val 155	Ala	Glu	Glu	Glu	Ala 160
25	Thr	Ser	Gly	Leu	Val 165	Met	Leu	Cys	Ile	His 170	Gly	Ser	Pro	Val	Asn 175	Ser
30	Tyr	Thr	Asn	Thr 180	Pro	Tyr	Thr	Gly	Ala 185	Leu	Gly	Leu	Leu	Asp 190	Phe	Ala
	Leu	Glu	Leu 195	Glu	Phe	Arg	Asn	Leu 200	Thr	Thr	Суз	Asn	Thr 205	Asn	Thr	Arg
35		210					215					220		Arg	_	
	Asp 225	Gly	Thr	Ala	Glu	Leu 230	Thr	Thr	Thr	Ala	Ala 235	Thr	Arg	Phe	Met	Lys 240
40	Asp	Leu	His	Phe	Thr 245	Gly	Leu	Asn	Gly	Val 250	Gly	Glu	Val	Gly	Arg 255	Gly

	Ile	Ala	Leu	Thr 260		Leu	Asn	Leu	Ala 265		Thr	Leu	Leu	Gly 270	Gly	Leu
5	Pro	Thr	Glu 275	Leu	Ile	Ser	Ser	Ala 280	Gly	Gly	Gln	Leu	Phe 285	Tyr	Ser	Arg
	Pro	Val 290		Ser	Ala	Asn	Gly 295	Glu	Pro	Thr	Val	Lys 300	Leu	Tyr	Thr	Ser
10	Val 305	Glu	Asn	Ala	Gln	Gln 310	Asp	Lys	Gly	Val	Ala 315	Ile	Pro	His	Asp	Ile 320
15	Asp	Leu	Gly	Asp	Ser 325	Arg	Val	Val	Ile	Gln 330	Asp	Tyr	Asp	Asn	Gln 335	His
	Glu	Gln	Asp	Arg 340	Pro	Thr	Pro	Ser	Pro 345	Ala	Pro	Ser	Arg	Pro 350	Phe	Ser
20	Val	Leu	Arg 355	Ala	Asn	Asp	Val	Leu 360	Trp	Leu	Ser	Leu	Thr 365	Ala	Ala	Glu
	Tyr	Asp 370	Gln	Ser	Thr	Tyr	Gly 375	Ser	Ser	Thr	Gly	Pro 380	Val	Tyr	Ile	Ser
25	Asp 385	Ser	Val	Thr	Leu	Val 390	Asn	Val	Ala	Thr	Gly 395	Ala	Gln	Ala	Val	Ala 400
30	Arg	Ser	Leu	Asp	Trp 405	Ser	Lys	Val	Thr	Leu 410	Asp	Gly	Arg	Pro	Leu 415	Pro
	Thr	Val	Glu	Gln 420	Tyr	Ser	Lys	Thr	Phe 425	Phe	Val	Leu	Pro	Leu 430	Arg	Gly
35	Lys	Leu	Ser 435	Phe	Trp	Glu	Ala	Gly 440	Thr	Thr	Lys	Ala	Gly 445	Tyr	Pro	Tyr
	Asn	Tyr 450	Asn	Thr	Thr	Ala	Ser 455	Asp	Gln	Ile	Leu	Ile 460	Glu	Asn	Ala	Ala
40	Gly 465	His	Arg	Val		Ile 470	Ser	Thr	Tyr		Thr 475	Arg	Leu	Gly		Gly 480

	Pro Val Ala Ile Ser Ala Ala Ala Val Leu Ala Pro Arg Ser Ala Leu 485 490 495	
. 5	Ala Leu Leu Glu Asp Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe 500 505 510	
	Asp Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln 515 520 525	
10	(2) INFORMATION FOR SEQ ID NO:29:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 43 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
20	(iii) HYPOTHETICAL: NO	
	<pre>(vi) ORIGINAL SOURCE: (C) INDIVIDUAL ISOLATE: HEV 5' primer</pre>	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
	GGGGGGGATC CATATGGCGG TCGCTCCGGC CCATGACACC CCG 43	
30	(2) INFORMATION FOR SEQ ID NO:30:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA	
40	(iii) HYPOTHETICAL: NO	

(vi) ORIGINAL SOURCE:

```
(C) INDIVIDUAL ISOLATE: HEV 3' primer
  5
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
         ATTAGAAGCT TCCGTGGCCA TTATATG
                                                                              27
         (2) INFORMATION FOR SEQ ID NO:31:
 10
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 33 amino acids
                   (B) TYPE: amino acid
                   (D) TOPOLOGY: linear
15
             (ii) MOLECULE TYPE: protein
            (iii) HYPOTHETICAL: YES
20
             (iv) ANTI-SENSE: NO
             (v) FRAGMENT TYPE: internal
             (vi) ORIGINAL SOURCE:
25
                   (C) INDIVIDUAL ISOLATE: internally consistent sequence of
                          two HEV 406.4-2 antigens
            (ix) FEATURE:
                   (A) NAME/KEY: Modified-site
30
                   (B) LOCATION: 3
                   (D) OTHER INFORMATION: /note= "where Xaa is Q or P"
           (ix) FEATURE:
                   (A) NAME/KEY: Modified-site
35
                   (B) LOCATION: 5
                  (D) OTHER INFORMATION: /note= "where Xaa is G or D"
           (ix) FEATURE:
                  (A) NAME/KEY: Modified-site
40
                  (B) LOCATION: 7
                  (D) OTHER INFORMATION: /note= "where Xaa is L or S"
```

	(ix) FEATURE:
	(A) NAME/KEY: Modified-site
	(B) LOCATION: 12
_	(D) OTHER INFORMATION: /note= "where Kaa is E or V"
5	
	(ix) FEATURE:
	(A) NAME/KEY: Modified-site
	(B) LOCATION: 13
10	(D) OTHER INFORMATION: /note= "where Xaa is I or T"
10	/irl PEAGURE.
	(ix) FEATURE:
	(A) NAME/KEY: Modified-site (B) LOCATION: 22
15	(D) OTHER INFORMATION: /note= "where Xaa is P or H"
	(ix) FEATURE:
	(A) NAME/KEY: Modified-site
	(B) LOCATION: 24
	(D) OTHER INFORMATION: /note= "where Xaa is A or V"
20	, , , , , , , , , , , , , , , , , , ,
	(ix) FEATURE:
	(A) NAME/KEY: Modified-site
	(B) LOCATION: 29
	(D) OTHER INFORMATION: /note= "where Xaa is P or L"
25	
	(ix) FEATURE:
	(A) NAME/KEY: Modified-site
	(B) LOCATION: 31
30	(D) OTHER INFORMATION: /note= "where Xaa is L or P"
30	
	(vi) SEQUENCE DESCRIPTION, GROUD NO. 21
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
	Ala Asn Xaa Pro Xaa His Xaa Ala Pro Leu Gly Xaa Xaa Arg Pro Ser
35	1 5 10 15
	Ala Pro Pro Leu Pro Xaa Val Xaa Asp Leu Pro Gln Xaa Gly Xaa Arg
	20 25 30
40	Arg